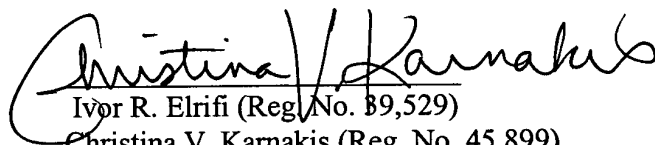


compliance with 37 C.F.R. §§ 1.821-1.825. The specification has been amended to correct typographical errors, to insert SEQ ID NOs and to insert the sequence listing.

The Commissioner is hereby authorized to charge any additional fees that may be due, or credit any overpayment of same, to Deposit Account No. 50-0311, Attorney Reference No. 21402-225 (Cura-525). Should any questions or issues arise concerning this application, the Examiner is encouraged to contact the undersigned at the telephone number provided below.

Respectfully submitted,

September 17, 2002



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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Table 1E was amended as follows:

Table 1E. Domain Analysis of NOV1			
<p><u>gnl Smart smart00042</u>, CUB, Domain first found in C1r, C1s, uEGF, and bone morphogenetic protein; This domain is found mostly among developmentally-regulated proteins. Spermadhesins contain only this domain.</p> <p>CD-Length = 114 residues, 99.1% aligned</p> <p>Score = 85.5 bits (210), Expect = 1e-17</p>			
Query:	799	CGGELGDTGYIESPNYPGDYPANAECVWHIAPPPKRRILIVVPEIFLPIEDECG-DVLV	857
		CGG L +G I SPNYP YP N CVW I+ PP RI + + L D C D +	
Sbjct:	1	CGGTLTASSGTITSPNYPNSYPNNLNCVWTISAPPGYRIELKFTDFDLESSDNCTYDYVE	60
Query:	858	MRKSASPTSITTYETCQTYERPIAFTSRSRKLWIQFKSNEGNSGKGFQVPYVT	910
		+ S +S C + P +S S + + F S+ +GF Y	
Sbjct:	61	IYDGPSTSSPLLGRFCGSELPPPIISSSSNSMTVTFVSDSSVQKRGSARYSA	113 (SEQ
ID NO: 181)			

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Table 2K on page 35 was amended as follows:

Table 2K. Domain Analysis of NOV2			
<p><u>gnl Smart smart00110</u>, C1Q, Complement component C1q domain.; Globular domain found in many collagens and eponymously in complement C1q. When part of full length proteins these domains form a 'bouquet' due to the multimerization of heterotrimers. The C1q fold is similar to that of tumour necrosis factor.</p> <p>CD-Length = 132 residues, 84.1% aligned Score = 86.7 bits (213), Expect = 1e-18</p>			
Query:	91	MAVTFDKVYVNIGGDFDAAAGVFRCLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMI	
	150		
		V FDKV N G +D + G F C +PG Y+FS+ + + + + V LMKN +V	
Sbjct:	20	QPVRFDKVLYNQQGHYDPSTGKFTCPVPGVYYFSYHI-ESKGRNVKVSLMKNGIQVMRE-	77
Query:	151	YDDGASRRREMQSQSVMALALRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVY	204
		D+ ++ S +L LR+GD VW L D G Y+ TFSGFL++	
Sbjct:	78	CDEYQKGLYQVASGGALLQLRQGDQVW-LELDDKKNGLYAGEEVDSTFSGFLLF	130 (SEQ
ID NO:	182)		

Table 3E Domain Analysis of NOV3			
gnl Smart smart00220, S_TKc, Serine/Threonine protein kinases, catalytic domain; Phosphotransferases. Serine or threonine-specific kinase subfamily.			
CD-Length = 256 residues, 100.0% aligned Score = 237 bits (605), Expect = 1e-63			
Query: 191	FSVHRIIGRGGFGEVYGCRKRD	TGKMYAMKCLDKKRIKMKQGETLALNERIMLSLVSTGD	250
	+ + ++G+G FG+VY R + TGK+ A+K + K+++K K+ E L E +L + D		
Sbjct: 1	YELLEVLGKGAFGKVYLARDKKTGKLV	AIKVIKKEKLKKKKRER-ILREIKILKKL---	D 56
Query: 251	CPFIVCMSYAFHTPDKLSFILDLMNGGDLHYHLSQHG	VFSEADMRFYAAEIILGLEHMHN	310
	P IV + F DKL +++ GDDL L + G SE + RFYA +I+ LE++H+		
Sbjct: 57	HPNIVKLYDVFEDDDKLYLVMEYCEGGDLFDLLKKR	GRLESEDEARFYARQILSALEYLHS	116
Query: 311	RFVVYRDLKPANILLDEHGHVRISDLGLACDFS	KKKPHAS--VGTHGYMAPEVLQKGVAY	368
	+ +++RDLKP NILLD GHV+++D GLA + VGT YMAPEVL G Y		
Sbjct: 117	QGIHRDLKPENILLDSDGHVKLADFG	LAKQLDSGGTLLTTFVGTPEYMAPEVL-LGKGY	175
Query: 369	DSSADWFSLGCMLFKLLRGHSPFRQHKT	KDK-HEIDRMTLTMAVELPDSFSPELHSLLEG	427
	+ D +SLG +L++LL G PF + SPE L++		
Sbjct: 176	GKAVDIWSLGVILYELLTGKPPFPGDDQLLALFKK	IGKPPPPPPPEWKISPEAKDLIKK	235
Query: 428	LLQRDVNRRLGCLGRGAQEVKESPFF	453	
	LL +D +RL A+E E PFF		
Sbjct: 236	LLVKDPEKRL-----TAE	EALHPFF 256 (SEQ ID NO: 183)	

Table 3E on page 45 has been amended as follows:

The paragraph following Table 3E on page 45 has been amended as follows:

[gi|5139484|FKEACRLRRAPKFLNKPRSGTVELPKPSLCHPNSNGI]

Table 4E on page 63 has been amended as follows:

Table 4E. Domain Analysis of NOV4	
<p>gnl Pfam pfam01500, Keratin_B2, Keratin, high sulfur B2 protein. High sulfur proteins are cysteine-rich proteins synthesized during the differentiation of hair matrix cells, and form hair fibers in association with hair keratin intermediate filaments. This family has been divided up into four regions, with the second region containing 8 copies of a short repeat. This family is also known as B2 or KAP1.</p>	
<p>CD-Length = 144 residues, 87.5% aligned Score = 38.9 bits (89), Expect = 0.004</p>	
Query: 630	CIDVACSNHGTCITGTCTCNPGYKGESCEEVDCMDPTCSGRGVCVRGECHCFVGWGGTNC
689	
Sbjct: 5	C CS GTC + C + SC + C P CS C R C + C
57	CGFPTCSTLGTCGSSCC-----QPPSCCQPSCCQPVCSQTTCC-RPTCFQSSCCRPSCC
Query: 690	ETP--RATCLDQCSGHGTFLPDTGLCSCDPSWTGHDCSIEICAADCGGHGVCVGGTCRCE
747	
Sbjct: 58	+T + TC S G+ SC W DC +E
93	QTSCCQPTCCQSSSCQ----TGCGIGSCRTRWCRPDCRVE-----
Query: 748	DGWMGAACDQRACHPRCAEHGTCRDGKCECS---PGWNGEHC 786
	C C C C+ + S P + G+ C
Sbjct: 94	-----GTCLPPCCVVSTPPTCCQPVSAQASCCRPSYCGQSC 130 (SEQ ID NO:
184)	

Table 6G on pages 84-85 has been amended as follows:

Table 6G. Domain Analysis of NOV6				
<p><u>gnl Pfam pfam01404</u>, EPH_lbd, Ephrin receptor ligand binding domain. The Eph receptors, which bind to ephrins pfam00812 are a large family of receptor tyrosine kinases. This family represents the amino terminal domain which binds the ephrin ligand.</p> <p>CD-Length = 174 residues, 100.0% aligned</p> <p>Score = 345 bits (886), Expect = 6e-96</p>				
Query:	33	QVLLDTSTVMGELGWKTYPLNGWDAITEMDEHNRPIHTYQVCNVMEPNQNNWLRTNWIS	92	
		+V LLDT+T GELGW TYP GW+ ++ +DE+NRPI TYQVCNVMEPNQNNWLRTNWI		
Sbjct:	1	EVTLLDTTTATGELGWLTYPGGWEEVSGLDENNRPIRTYQVCNVMEPNQNNWLRTNWIP	60	
		o o o o o o		
Query:	93	RDAAQKIYVEMKFTLRDCNSIPWVLGTCKETFTLYYIESDESHGTFKFKPSQYIKIDTIAA	152	
		R AQ++YVE+KFT+RDCNS+P VLGTCKETF LYY ESDE G ++ +QY K+DTIAA		
Sbjct:	61	RRGAQRVYVELKFTVRDCNSLPGVLGTCKETFNLYYYESDEDVGPWRENQYTKVDTIAA	120	
Query:	153	DESFTQMDLGDRILKLNTEIREVGPIERKGFYLAQFDIGACIALVSVRVFYKKC	206	
		DESFTQ+DLGDR++KLNTE+R VGP+ +KGFYLAQD+GAC+ALVSVRVFYKKC		
Sbjct:	121	DESFTQVDLGDRVMKLNTEVRSVGPLSKKGFYLAQDVGACMALVSVRVFYKKC	174	(SEQ
	ID NO: 185)			

Table 7E on pages 92-93 has been amended as follows:

Table 7E. Domain Analysis of NOV7					
gnl Pfam pfam00083, sugar_tr, Sugar (and other) transporter.					
CD-Length = 447 residues, 96.6% aligned					
Score = 246 bits (629), Expect = 2e-66					
Query:	21	FQVFKSFYNETYFERHATFM----	DGKLMLLWSCTVSMFPLGGLLGSLLVGLLVDS	CGR	76
		V F F +	+L VS+F +G +GSL G L D GR		
Sbjct:	16	TGVIGGFATLIDFLFFFGGLTSSGSCAESTVLSGLVVS	IFFVGRPIGSLFAGKLGDRFGR		75
Query:	77	KGTLLINNIFAIIPAILMGVSKVAKAFELIVFSRVVLGVCAGISYSALPMYLGELAPKNL			136
		K +LLI + +I ++L G++ A F L++ RV++G+ G + +PMY+ E+APK L			
Sbjct:	76	KKSLLIGLVLFVIGSLLSGLAPGA--FYLLIVGRVLVGLGVGGASVLVPMYISEIAPKAL			133
Query:	137	RGMVGTMTTEVFVIVGVFLAQIFSLQAILGNPAGWPVLLALTGVPALLQLLTLPFFPESPR			196
		RG +G++ ++ + +G+ +A I L N GW + L L VPALL L+ L F PESPR			
Sbjct:	134	RGALGSLYQLGITIGILVAAIIGLGLNKTNNWGWRIPLGLQLVPALLLIGLLFLPESPR			193
Query:	197	YSLIQKGDEATARPLRRLRGHTDMEAELEDMAEARAERAEGHLSVLHLCALRSLRWQLL			256
		+ +++ E L +LRG D++ E+++ +AE A + + R +LL			
Sbjct:	194	WLVKLGKLEEARAVLAKLRGVEDVDQEIQEEKAELEAGVSSEKAGLELF--RGRTRQRLL			251
Query:	257	SIIVLMAGQQLSGINAINYYADTIYTSAGVEAAHSQYVTVGSGVVNIVMTITSVVLVERL			316
		++L QQL+GINAI YY+ TI+ S G+ + + VT+ GVVN V T ++ LV+R			
Sbjct:	252	MGVMLQIFQQLTGINAIIFYSPTIFKSVGMSDSVALLVTIIVGVNFFVATFVAIFLVDRF			311
Query:	317	GRRHLLLAGYGICGSACLVLTVPSPPPQNRVPELSYLGIIICVFAYIAGHSIGPSPVPSVVR			376
		GRR LLL G L+L V+ P + I+ + +IA ++G P+P V+			
Sbjct:	312	GRRPLLLLGAAGMAICFLILGVA-LLLLNKPAGIVAIVFILLFIAFFALGWGPIPWIL			370
Query:	377	TEIFLQSSRRAAFVMDGAVHWLTNFIIGFLFPSIQEAIG-AYSFIIFAGICLLTAIYIYV			435
		+E+F R A + A +WL NFIIGFLFP I AIG Y F+ FAG+ +L +++Y			
Sbjct:	371	SELFPTGVRSKAMALATAANWLANFIIGFLFPYITGAIGGGYVFLFFAGLLVLFILFVYF			430
Query:	436	VIPETKGKTFVEINRIF			452
		+PETKG+T EI+ +F			
Sbjct:	431	FVPETKGRITLEEIDELF			447 (SEQ ID NO: 186)

Table 8E on page 101 has been amended as follows:

Table 8E. Domain Analysis of NOV8			
gnl Smart smart00179, EGF_CA, Calcium-binding EGF-like domain			
CD-Length = 41 residues, 80.5% aligned			
Score = 52.8 bits (125), Expect = 7e-08			
Query:	125	DIDCEVSGLCRHGGRCVNTGHSFECY-CMDGY	156
		DIDEC C++GG CVNT GS+ C C GY	
Sbjct:	1	DIDECASGNPCQNGGTCVNTVGSYRCEECPPGY	33 (SEQ ID NO: 187)

Table 9E on page 109 has been amended as follows:

Table 9E. Domain Analysis of NOV9			
gnl Smart smart00179, EGF_CA, Calcium-binding EGF-like domain			
CD-Length = 41 residues, 80.5% aligned			
Score = 52.8 bits (125), Expect = 7e-08			
Query:	125	DIDCEVSGLCRHGGRCVNTGHSFECY-CMDGY	156
		DIDEC C++GG CVNT GS+ C C GY	
Sbjct:	1	DIDECASGNPCQNGGTCVNTVGSYRCEECPPGY	33 (SEQ ID NO: 188)

Table 10E on page 116 has been amended as follows:

Table 10G Domain Analysis of NOV10			
<u>gnl Smart smart00409</u> , IG, Immunoglobulin			
CD-Length = 86 residues, 89.5% aligned			
Score = 37.0 bits (84), Expect = 0.001			
Query: 27	SNVTLECNFDTGSHVNLGAITVSLQKVENDTSPHRERATLLEEQLPLGKASFHIPQVQVR	86	
	+VTL C TV+ K R ++ G ++ I V		
Sbjct: 10	ESVTLSCASGNPPP-----TVTWYKQGKLLAESGRFSVSRSG---GNSTLTISNVTPE	61	
Query: 87	DEGQYQCIIYGVAWDYKYLTLKVK	111	
	D G Y C TL V		
Sbjct: 62	DSGTYTCAATNSSGSASSGTTLTVL	86	(SEQ ID NO: 189)

Table 11E on page 123 has been amended as follows:

Table 11E. Domain Analysis of NOV11			
<u>gnl Smart smart00406</u> , IGv, Immunoglobulin V-Type			
CD-Length = 80 residues, 96.2% aligned			
Score = 34.7 bits (78), Expect = 0.008			
Query: 52	VELQCQLFPNISAEDMELRWYRCQPSLAVHMERGMDMDGEQKWQYRGRTTFMSDHVARG	111	
	V L C+ + W R P + + Y+GR T D+ ++		
Sbjct: 2	VTLSCKASGF-TFSSYYVSWVRQPPGKGLEWLGYIGSDVSYSEASYKGRVTISKDN-SKN	59	
Query: 112	KAMVRSHRVTTFDNRTYCC	130	
	+ + D TY C		
Sbjct: 60	DVSLTISNLRVEDTGTYYC	78	(SEQ ID NO: 190)